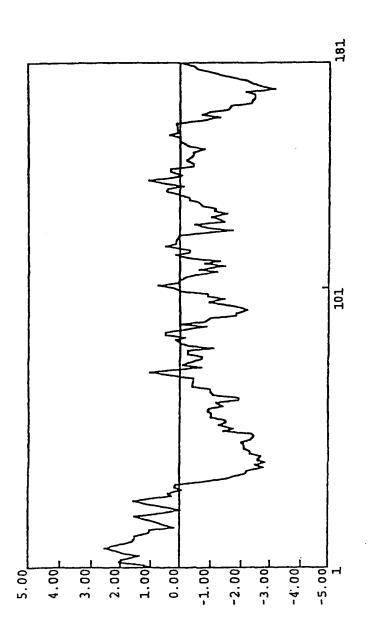
			9	•		18			27			36			45		mc à	54
5 י	ATG	GAA	ATT	TTA	TCA	TCA	AAA	CTA	TTC	ATT	TTA	TTG	ACT	TTA	GCC	ACT	TCA	AGC
	Met	Glu	Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser
			63		•	72			81			90			99			108
	TTG	TTA	ACA	TCA	AAC	ATT	TTT	TGT	GCA	GAT	GAA	TTA	GTG	ATG	TCC	AAT	CIT	CAC
	Leu	Leu	Thr	Ser	ASD	116	Pne	Cys	MIA	veh	GIU	Deu	YUL	1100				His
			117			126			135			144			153			162
	AGC	AAA	GAA	AAT	TAT	GAC	AAA	TAT	TCT	GAG	CCT	AGA	GGA	TAC	CCA	AAA	GGG	GAA
			C3.13	Aen	Tyr	Asp	Lvs	Tvr	Ser	Glu	Pro	Arg	Gly	Tyr	Pro	Lys	Gly	Glu
	Ser	цуs	GIU	nsu	-1-			-2					_	_				216
			171			180	<i>~</i>	CDCT N	189	Chm	TCC.	198	CCA	AAA	207	GTT	ATT	
										~ ~ ~								
	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys
	-								243			252			261			270
	»mc	λCT	225 ACA	CCT	GCA	234 GTC	AAT	AAA	ATG	CCA	CAC	TCC	TTC	GCC	AAC	TTG	CCA	TTG
													_					
	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys	Met	Pro	HIS	ser	Pne	Ald	ASII	Leu	FIO	1 00
			279			288			297			306			315			324
	AGA	TTT	GGG	AGG	AAC	GTT	CAA	GAA	GAA	AGA	AGT	GCT	GGA	GCA	ACA	GCC	AAC	CTG
				7	7	 V= 1	Gln	Glu	Glu	Ara	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu
	Arg	Pne	GrĀ	w1.a	กอน	Val				,			•					
			333			342			351	CTDC	200	360	CTC) C)	369	ىلىش	CCT	378 AAC
																GTT		
	Pro	Leu	Arg	Ser	Gly	Arg	Asn	Met	Glu	Val	Ser	Leu	Val	Arg	Arg	Val	Pro	Asn
					_							414			423			432
	OTTC:	ccc	387	AGG	ىلملىك	396 GGG	AGA	ACA	405 ACA	ACA	GCC	AAA	AGT	GTC		AGG	ATG	
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu
			441			450			459			468			477			486
	AGT	GAT	TTG	TGT	CAA	GGA	TCC	ATG	CAT	TCA	CCA	TGT	GCC	AAT	GAC	ATT	TTT	TAC
	Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ата	ASII	ASP	Leu	PIIC	TYL
			495	•		504			513			522			531			540
	TCC	ATG	ACC	TGC	CAG	CAC	CAA	GAA	ATC	CAG	AAT	CCC	GAT	CAA	AAA	CAG	TCA	AGG
														-				
	Ser	Met	Thr	Cys	Gln	His	Gln	GIU	TTE	GTD	ASD	PLO	waħ	GTII	n y o	Gln		<i>,</i> — ¬

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Fig.2



5'	ATG	GAA	9 ATT	ATT	TCA						' TTA		ACI				TCA	54 AGC
	 Met	Glu	Ile	 Ile	 Ser	 Ser	 Lys	Leu	 Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser
				TCA			TTT			GAT			GTG	~		AAT		108 CAC
	AGC	AAA 	117 GAA	AAT	TAT	126 GAC	AAA	TAT	135 TCT	GAG	CCT	144 AGA	GGA	TAC	153 CCA	. AAA 	GGG	162 GAA
	Ser	Lys			Тух			Tyr			Pro		Gly	Тух			Gly	
	AGA	AGC	171 CTC		TTT	180 GAG		TTA	189 AAA		TGG	198 GGA	CCA	AAA	207 AAT		ATT	216 AAG
	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Ąsp	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys
	ATG	AGT	225 ACA	CCT	GCA	234 GTC	AAT	AAA	243 ATG	CCA	CAC	252 TCC	TTC	GCC	261 AAC		CCA	270 TTG
	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys	Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu
													GGA					
	Arg	Phe	Gly	Arg	Asn	Val	Gln	Glu	Glu	Arg	Ser		Gly	Ala			Asn	Leu
						AGA		ATG		GTG			GTG			GTT 		
	Pro	Leu	Arg	Ser	Gly		Asn	Met			Ser		Val	Arg		Val	Pro	
	CTG	CCC	387 CAA	AGG	TTT	396 GGG	AGA	ACA	405 ACA		GCC	414 AAA	AGT	GTC	423 TGC	AGG	ATG	432 CTG
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu
	AGT	GAT	441 TTG	TGT	CAA	450 GGA	TCC	DTA	459 CAT	TCA	CCA	468 TGT	GCC	AAT	477 GAC	TTA	TTT	486 TAC
	Ser	Asp	Leu	Cys	Gln	GJÀ	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	Phe	Tyr
	TCC	ATG	495 ACC	TGC	CAG	504 CAC	CAA	GAA	513 ATC	CAG	AAT	522 CCC	GAT	CAA	531 AAA	CAG	TCA	540 AGG
	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	Gln	Lys	Gln	Ser	Arg
	AGA	CIG	549 CTA	TTC	AAG	558 AAA	ATA	GAT	567 GAT	GCA	GAA	576 TTG	AAA	CAA	585 GAA	AAA	TAA	3'
	Arg	Leu	Leu	Phe	Lys	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***	

5,	ATG	GAA	9 ATT	ATT	TCA	18 TTA	AAA	CGA	27 TTC	ATT	TTA	36 TTG	DTA	TTA	45 GCC		TCA	54 AGC
•			 Ile															
	TTG	TTA	63 ACA	TCA	AAC	72 ATC	TTC	TGC	81 ACA	GAC	GAA	90 TCA	AGG	ATG	99 CCC	AAT	CTT	108 TAC
			Thr															
	AGC	AAA	117 AAG	TAA	TAT	126 GAC	AAA	TAT	135 TCC	GAG	CCT	144 AGA		GAT	153 CTA	GGC	TGG	162 GAG
	 Ser	 Lys	 Lys	 Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Asp	Leu	Gly	Trp	Glu
	AAA	GAA	171 AGA	agt	CTT	180 ACT	TTT	GAA	189 GAA	GTA	AAA	198 GAT	TGG	GCT	207 CCA		ATT	216 AAG
	 Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val	Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys
	ATG	ААТ	225 AAA	CCT	GTA	234 GTC	AAC	AAA	243 ATG	CCA	CCT	252 TCT	GCA	GCC	261 AAC	CTG	CCA	270 CTG
	Met	asn	 Lys	Pro	Val	Val	Asn	Lys	Met	Pro	Pro	Ser	Ala	Ala	Asn	Leú	Pro	Leu
			279 GGG															
	Arg	Phe	Gly	Arg	Asn	Met	Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu
			333 AGA Arg							GAC		CTC		AGA				
			387			396			405			414			423			432
	CTG	CCC	CAG	AGG	TTT	GGA	AGA	ACA	ACA	ACA	GCC	AAA 	AGC	ATT	ACC	AAG 	ACC	CTG
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu
	AGT	ААТ	441 TTG	CTC	CAG	450 CAG	TCC	ATG	459 CAT	TCA	CCA					CTA		486 TAC
	Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	GJÀ	Leu	Leu	Tyr
	TCC	ATG	495 GCC	TGC	CAG	504 CCC	CAA	GAA	513 ATC	CAG	TAA		GGT	CAA	531 AAG	AAC	CTA	540 AGG
	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln	Lys	Asn	Leu	Arg
	AGA	CGG	549 GGA	TTC	CAG	558 AAA	ATA	GAT	567 GAT	GCA	GAA	576 TTG	AAA	CAA	585 GAA	AAA 	TAA 	3'
	Arg	Arg	Gly	Phe	Gln	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***	

ATG	GAA	9 TTA /			18 TCA			27 TTC						45 GCA		TCA	54 AGC
Me t	Glu	lle	Ile	Ser		Lys	Arg			Leu			Leu		Thr	Ser	
ттс	TTA	63 ACT	TCA	AAC	72 ACC	CTT	TGT	81 TCA		GAA	90 TTA		ATG	99 CCC	CAT	TTT	108 CAC
—– Phe	 Leu	Thr	 Ser	 Asn	Thr	 Leu	 Cvs	 Ser	Asp	 Glu	Leu	 Mel	 Me t	—— Рго	 His	 Phe	His
		117			126			135			144			153	••••		162
AGC	AAA	GAA	GGT	TAT	GGA	AAA	TAT	TAC	CAG	GTG	AGA	GGA	ATC	CCA	AAA	GGG	GTA
Ser	Lys	Giu 171	Gly	Tyr	Gly 180	Lys	Tyr				Arg 198		Ile	Pro 207	Lys	Gĺy	Val 216
AAG	GAA	AGA	AGT	GTG	ACT	TTT	CAA						GGG		AAG	AAA	GAT
Lys	Glu	Arg 225	Ser	Val	Thr 234	Phe	Gln	Glu 243		Lys		Trp	Gly	Ala 261	Lys	Lys	Asp 270
ATT	AAG	ATG	AGT	CCA		CCT	GCC					CAC	TCA		GCC	AAC	
Ile	Lys	Me t 279	Ser	Pro	Ala 288			Asn 297				His	Ser	Ala 315	Ala	Asn	Leu 324
CCC	CTG	AGG	TTT	GGG								AGC	CCC		GCA	CGG	
Pro	Leu	Arg 333	Phe		Arg 342		Ile		Asp		Arg 360	Ser	Pro	Arg 369	Ala	Arg	Ala 378
AAC	ATG	GAG	GCA	GGG	ACC	ATG	AGC	CAT	TTT	CCC	AGC	CTG	CCC	CAA	AGG	TTT	GGG
Asn	Met	Glu 387	Ala		Thr 396	Met		His 405	Phe		Ser 414	Leu	Pro	Gln 423	Arg	Phe	Gly 432
AGA	ACA	ACA	GCC	AGA	CGC	ATC	ACC	AAG	ACA	CTG	GCT	GGT	TTG	CCC	CAG	AAA	TCC
Arg	Thr	Thr 441	Ala		Arg 450			Lys 459			Ala 468			Pro 477	Gin	Lys	Ser 486
CTG	CAC	TCC	CTG	GCC	TCC										CAG	CAT	
Leu	His	Ser 495	Leu		Ser 504	Ser		Ser 513	Leu		Ala 522	Me t		Arg 531	Gln		Gin 540
GAA A	TTA	CAG	AGT	CCT	GGT	CAA			CCT			CGC			ACG		
Glu :	Ile	Gl n 549	Ser :		 Glу 558	Gln		 Gln 567	Pro		Lys 576	Arg		 Phe 585	Thr		 Thr 594
AT (GAT	GCA	GAA .			CAA			ATA			СТС			GTC		
lsp /		Ala 603	Glu .		 Lys : 612	Gln	Glu :	Lys	Ile	 Gly	As n	Leu	Gln	Pro	Val	 Leu	Gln
GG (ATG .	AAG (3,											
	la	Me l	Lys i	Leu :	+ * *					•							

METISSMET ILMANSSIL TSNIEGADEL WENTHSKEN YDKYSEPRG- METISSKRFT ILMANSSIL TSNIEGADEL WENTHSKEN YDKYSEPRG- METISSKRFT ILMANSSIL TSNIEGADEL WENTHSKEN YDKYSEPRG- METISSKRFT ILMANSSIL TSNIEGADES RAPNINGSKR YDKYSEPRG- METISSKRFT ILMANSSIL TSNIEGADE PRANKAREG WENTHSKEN WENTHSKEN WENTHSKEN WENTHSKEN WENTHSKEN GENAVIKASIT FANNKAREG WENTHSKEN SILGENER STREETKOM APK-IRAGE AND PARKYCKN SILGENER SILGENER SWENTHSKEN AND PARKYCKN TAKSYCKMF SILGENER AND SILGENER SWENTHSKEN AND SILGENER AND SILGENER SWENTHSKEN AND SILGENER AND SILGENER STREETKEN GENASHER SILGENER TAKSYCKMF SILGENER AND SILGENER SWENTHSKEN AND SKRUNG SKRU
10 NEITSSKIFT LIMIATSSIL TSNIFC 1 NEITSSKIFT LIMIATSSIL TSNIFC 1 NEITSSKRFT LIMIATSSFL TSNIFC 51 LGWEK-ER SINFEELKOW GPRAVI 52 LGWEK
1 MEIISSKIFT 1 1 MEIISSKRFT 1 1 MEIISSKRFT 1 51 — YPKG-ER 51 LGWEK-ER 51 LGWEK-ER 51 100 PKGVKER 60 101 MEEERSAGAT 110 MEETSAGAT 11
101 101 101 101 101 151 151 151 201 201
hLPLRF. aa bLPLRF. aa hLPLRF. aa rLPLRF. aa rLPLRF. aa bLPLRF. aa rLPLRF. aa bLPLRF. aa rLPLRF. aa rLPLRF. aa rLPLRF. aa rLPLRF. aa rLPLRF. aa

58	TTTAGACTTAGACGAAATGGAAATTATTTCATTAAAACGATTCATTTTATTGACTGTG	1
14	MetGluIleIleSerLeuLysArgPheIleLeuLeuThrVal	1
118	GCAACTTCAAGCTTCTTAACATCAAACACCTTCTGTACAGATGAGTTCATGATGCCTCAT	59
34	AlaThrSerSerPheLeuThrSerAsnThrPheCysThrAspGluPheMetMetProHis	15
178	TTTCACAGCAAAGAAGGTGACGGAAAATACTCCCAGCTGAGAGGAATCCCAAAAGGGGAA	119
54	PheHisSerLysGluGlyAspGlyLysTyrSerGlnLeuArgGlyIleProLysGlyGlu	35
238	AAGGAAAGAAGTGTCAGTTTTCAAGAACTAAAAGATTGGGGGGCAAAGAATGTTATTAAG	179
74	LysGluArgSerValSerPheGinGluLeuLysAspTrpGlyAlaLysAsnValIleLys	55
298	ATGAGTCCAGCCCCTGCCAACAAGTGCCCCACTCAGCAGCCAACCTGCCCCTGAGATTT	239
94	MetSerProAlaProAlaAsnLysValProHisSerAlaAlaAsnLeuProLeuArgPhe	75
358	GGAAGGACCATAGATGAGAAAAGAAGCCCCGCAGCACGGGTCAACATGGAGGCAGGGACC	299
114	GlyArgThrIleAspGluLysArgSerProAlaAlaArgValAsnMetGluAlaGlyThr	95
418	AGGAGCCATTTCCCCAGCCTGCCCCAAAGGTTTGGGAGAACAACAGCCAGAAGCCCCAAG	359
154	ArgSerHisPheProSerLeuProGinArgPheGiyArgThrThrAlaArgSerProLys	115
538	ACACCCGCTGATTTGCCACAGAAACCCCTGCACTCACTGGGCTCCAGCGAGTTGCTCTAC	419
154	ThrProAlaAspLeuProGlnLysProLeuHisSerLeuGlySerSerGluLeuLeuTyr	135
538	GTCATGATCTGCCAGCACCAAGAAATTCAGAGTCCTGGTGGAAAGCGAACGAGGAGAGGA	179
174	ValMetIleCysGlnHisGlnGluIleGlnSerProGlyGlyLysArgThrArgArgGly	155
598	GCGTTTGTGGAAACAGATGATGCAGAAAGGGAAACCAGAAAAATAGGAAACTCGAGCCCG	539
188	AlaPheValGluThrAspAspAlaGluArgLysProGluLys***	175
618	ACTTCAAGAGGCTACGGAGC	599
188		188

Fig.8

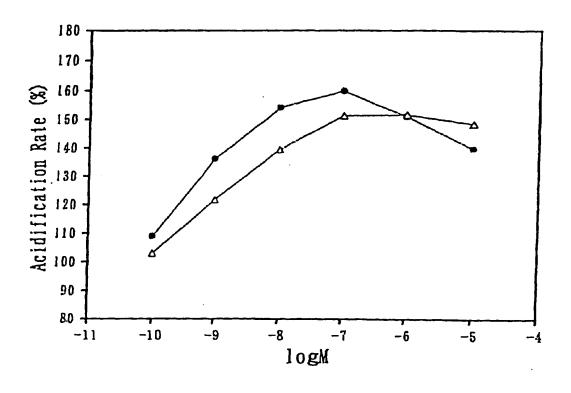
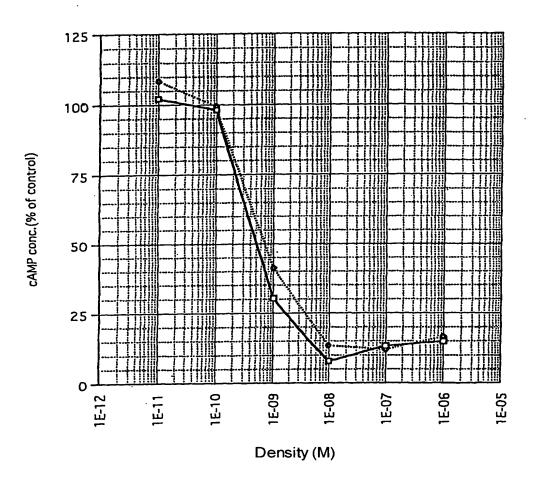


Fig.9



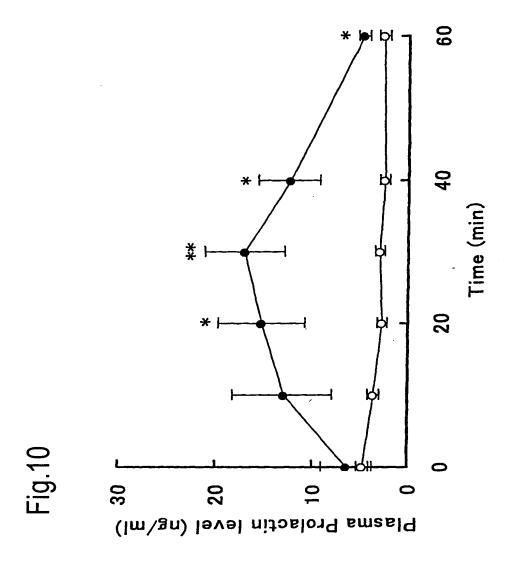


Fig.11

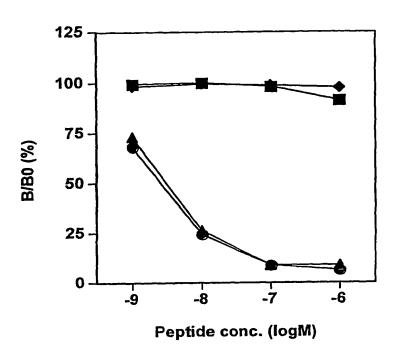


Fig.12

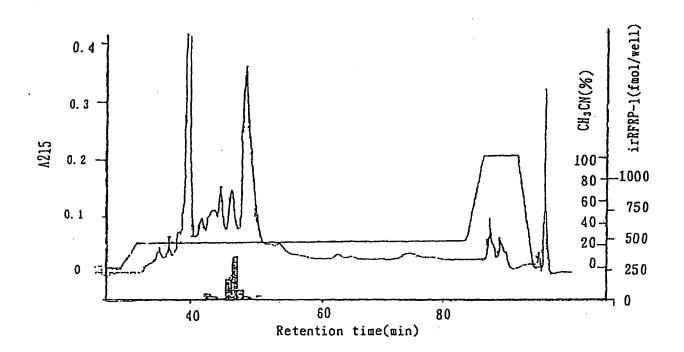


Fig.13

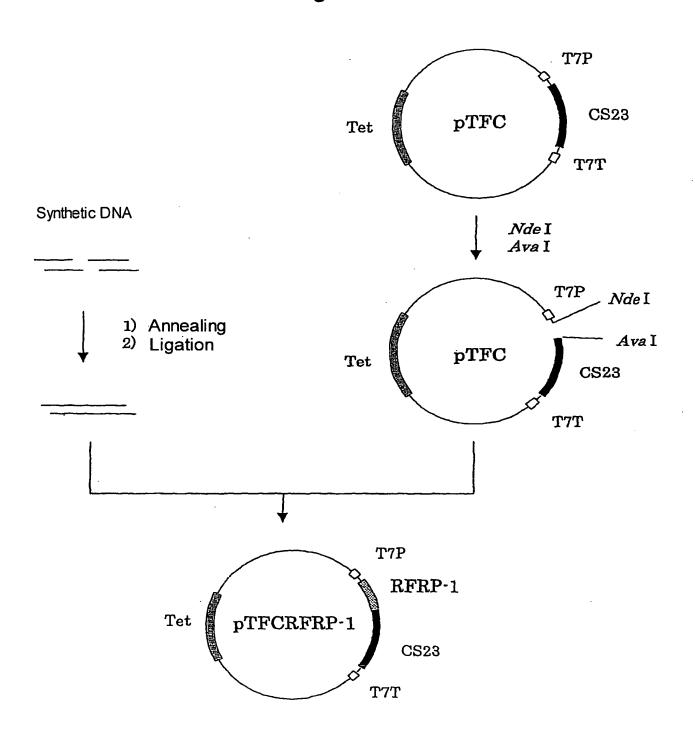


Fig.14

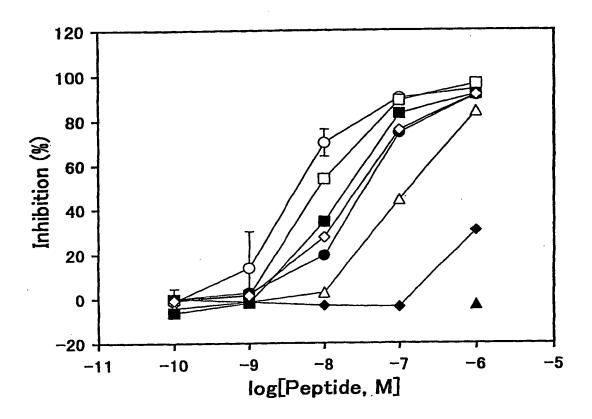


Fig.15

